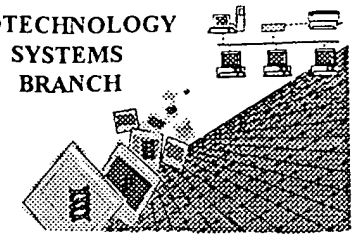
BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/026,106B
Source: OIPE
Date Processed by STIC: 8/29/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
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Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/026,106

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 ✓	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING DATE: 08/29/2002
PATENT APPLICATION: US/10/026,106B TIME: 13:29:11

Input Set : A:\EP.txt
Output Set: N:\CRF3\08292002\J026106B.raw

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Renauld, Jean-Christophe
2 Fickensicher, Helmut
3 Dumoutier, Laure
4 Hor, Simon
6 <120> TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2
8 <130> FILE REFERENCE: LUD 5752 NDH
C--> 10 **<140> CURRENT APPLICATION NUMBER: US/10/026,106B**
12 <141> CURRENT FILING DATE: 2001-12-21
14 <160> NUMBER OF SEQ ID NOS: 19

ERRORED SEQUENCES

42 <210> SEQ ID NO: 4
43 <211> LENGTH: (20) 19 shown
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
W--> 46 **<220> FEATURE:**
W--> 47 **<400> SEQUENCE: 4**
E--> 48 **cagaaggtca gtgctgaag** (20) 19
66 <210> SEQ ID NO: 7
67 <211> LENGTH: 1599
68 <212> TYPE: DNA
69 <213> ORGANISM: Homo sapiens
W--> 70 **<220> FEATURE:**
W--> 71 **<400> SEQUENCE: 7**
73 aaggccatgg cggggcccga gcgctggggc cccctgctcc tgtgcctgct gcaggccgct 60
74 ccagggaggc cccgtctggc ccctccccag aatgtgacgc tgctctccca gaacttcagc 120
75 gtgtacctga catggctcc cagggcttggc aacccccagg atgtgaccta ttttgtggcc 180
76 atcagagctc tcccacccgt agacggtggc gcgaagtgga agagtgtgcg ggaaccaagg 240
77 agctgctatg ttctatgatg tgcctgaaga aacaggacct gtacaacaag ttcaagggac 300
78 gcgtgcggac ggtttctccc agctccaagt ccccctgggt ggagtccgaa tacctggatt 360
E--> 79 **acctttttga agtggagccg gccccacctg tcctggtgct cacccagacg gaggagatc** (420) 419
E--> 80 **ctgagtgcca atgccacgta ccagctgccc ccctgcatgc ccccactgga tctgaagtat** 480
E--> 83 **gaggtggcat tctggaagga gggggccgga aacaagaccc tatttccagt cactccccat** 540
E--> 84 **ggccagccag tccagatcac tctccagcca gctgccagcg aacaccactg cctcagtgcc** 600
E--> 85 **agaaccatct acacgttcag tgtcccgaaa tacagcaagt tctctaagcc cacctgcttc** 660
E--> 86 **ttgctggagg tcccagaagc caactgggct ttcctggtgc tgccatcgct tctgatactg** 720
E--> 87 **ctgttagtaa ttgccgcagg gggtgtgatc tggaagaccc tcatggggaa cccctggttt** 780
E--> 88 **cagcgggcaa agatgccacg ggccctggac ttttctggac acacacaccc tgtggcaacc** 840
E--> 89 **tttcagccca gcagaccaga gtccgtgaat gacttgttcc tctgtcccca aaaggaactg** 900
E--> 90 **accagagggg tcaggccgac gcctcgagtc agggccccag ccacccaaca gacaagatgg**
E--> 91 (960)

nos. off

make up - see item 1 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 08/29/2002
PATENT APPLICATION: US/10/026,106B TIME: 13:29:11

Input Set : A:\EP.txt
Output Set: N:\CRF3\08292002\J026106B.raw

```
E--> 92 aagaaggacc ttgcagagga cgaagaggag gaggatgagg aggacacaga agatggcgtc
E--> 93 1020
E--> 94 agcttccagc cctacattga accaccttct ttcctggggc aagagcacca ggctccaggg 1080
E--> 95 cactcggagg ctggtggggt ggactcaggg aggcccaggg ctcctctggt cccaagcgaa 1140
E--> 96 ggctcctctg cttgggattc ttcagacaga agctgggcca gcactgtgga ctcctcctgg 1200
E--> 97 gacagggctg ggtcctctgg ctatttggct gagaaggggc caggccaagg gccgggtggg
E--> 98 1260
E--> 99 gatgggcacc aagaatctct cccaccacct gaattctcca aggactcggg tttcctggaa 1320
E--> 100 gagctcccag aagataacct ctcctcctgg gccacctggg gcaccttacc accggagccg 1380
E--> 101 aatctggtcc ctgggggacc cccagtttct cttcagacac tgaccttctg ctgggaaagc 1440
E--> 102 agccctgagg aggaagagga ggcgagggaa tcagaaattg aggacagcga tgcgggcagc
E--> 103 1500
E--> 104 tgggggggctg agagcaccca gaggaccgag gacaggggcc ggacattggg gcattacatg
E--> 105 1560
E--> 106 gccaggtgag ctgtcccccg acatcccacc gaatctgatg 1600
     109 <210> SEQ ID NO: 8
     110 <211> LENGTH: 522
     111 <212> TYPE: PRT
     112 <213> ORGANISM: Homo sapiens
W--> 113 <220> FEATURE:
W--> 114 <400> SEQUENCE: 8
     115 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
E--> 116 1               5               10                  15
E--> 117
     118 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
E--> 119                    20                              25
E--> 120 30
     121 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
E--> 122                35                              40
E--> 123 45
     124 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
E--> 125         50                              55                  60
     126 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
E--> 127 65                              70                          75
E--> 128 80
     129 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 132                           85                              90
E--> 133 95
     134 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 135                    100                             105
E--> 136 110
     137 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 138             115                             120
E--> 139 125
     140 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 141        130                             135                 140
     142 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 143 145                           150                         155
E--> 144 160
```

nos. off and more cumulative totals up on line

522 S/2 shown

misaligned amino acid numbering

all item 3 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 08/29/2002
PATENT APPLICATION: US/10/026,106B TIME: 13:29:11

Input Set : A:\EP.txt
Output Set: N:\CRF3\08292002\J026106B.raw

```
     145 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 146                                165                             170
E--> 147 175
     148 Pro His Val Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro
E--> 149                        180                             185
E--> 150 190
     151 Ala Ala Ser Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe
E--> 152                195                             200                 205
     153 Ser Val Pro  Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu
E--> 154         210                             215                 220
     155 Glu Val Pro Glu Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu
E--> 156 225                             230                         235
E--> 157 240
     158 Ile Leu Leu Leu Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu
E--> 159                                245                     250
E--> 160 255
     161 Met Gly Asn Pro Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp
E--> 162                        260                             265
E--> 163 270
     164 Phe Ser Gly His Thr Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg
E--> 165                275                             280                 285
     166 Pro Glu Ser Val Asn Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr
E--> 167         290                             295                 300
     168 Arg Gly Val Arg Pro Thr Pro Arg Val Arg Pro Ala Thr Gln Gln Thr
E--> 169 305                             310                         315
E--> 170 320
     171 Arg Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Thr Glu
E--> 172                                325                             330
E--> 173 335
     174 Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly
E--> 175                        340                             345
E--> 176 350
     177 Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser
E--> 178                355                             360                 365
     179 Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp
E--> 180         370                             375                 380
     181 Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp
E--> 182 385                             390                         395
E--> 183 400
     186 Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly
E--> 187                            405                             410
E--> 188 415
     189 Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser
E--> 190                        420                             425
E--> 191 430
     192 Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser
E--> 193                435                             440
E--> 194 445
     195 Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Pro Asn Leu Val Pro
```

same end

RAW SEQUENCE LISTING DATE: 08/29/2002
PATENT APPLICATION: US/10/026,106B TIME: 13:29:11

Input Set : A:\EP.txt
Output Set: N:\CRF3\08292002\J026106B.raw

```
E--> 196       450                                 455                                 460
     197 Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser
E--> 198 465                                 470                                 475
E--> 199 480
     200 Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser
E--> 201                                 485                                 490
E--> 202 495
     203 Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg
E--> 204                         500                                 505
E--> 205 510
     206 Gly Arg Thr Leu Gly His Tyr Met Ala Arg                  515
E--> 207 520
     209 <210> SEQ ID NO: 9
     210 <211> LENGTH: 1469
     211 <212> TYPE: DNA
     212 <213> ORGANISM: Homo sapiens
W--> 213 <220> FEATURE:
W--> 214 <400> SEQUENCE: 9
     216 aaggccatgg cggggcccga gcgctggggc cccctgctcc tgtgcctgct gcaggccgct     60
     217 ccagggaggc cccgtctggc ccctccccag aatgtgacgc tgctctccca gaacttcagc   120
     218 gtgtacctga catggctccc agggcttggc aacccccagg atgtgaccta ttttgtggcc   180
     219 tatcagagct ctcccacccg tagacggtgg cgcgaagtgg aagagtgtgc gggaaccaag   240
     220 gagctgctat gttctatgat gtgcctgaag aaacaggacc tgtacaacaa gttcaaggga   300
     221 cgcgtgcgga cggtttctcc cagctccaag tccccctggg tggagtccga atacctggat   360
     222 taccttttg aagtggagcc ggccccacct gtcctggtgc tcacccagac ggaggagatc   420
     223 ctgagtgcca atgccacgta ccagctgccc ccctgcatgc ccccactgga tctgaagtat   480
     224 gaggtggcat tctggaagga gggggccgga aacaagaccc tatttccagt cactccccat   540
     225 ggccagccag tccagatcac tctccagcca gctgccagcg aacaccactg cctcagtgcc   600
     226 agaaccatct acacgttcag tgtcccgaaa tacagcaagt tctctaagcc cacctgcttc   660
     227 ttgctggagg tcccaggact tttctggaca cacacaccct gtggcaacct ttcagcccag   720
     228 cagaccagag tccgtgaatg acttgttcct ctgtccccaa aaggaactga ccagaggggt   780
E--> 229 caggccgacg cctcgagtca gggccccagc cacccaacag acaagatgga agaaggacct
     230 840
E--> 233 tgcagaggac gaagaggagg aggatgagga ggacacagaa gatggcgtca gcttccagcc
     234 900
     235 ctacattgaa ccaccttctt tcctggggca agagcaccag gctccagggc actcggaggc   960
     236 tggtggggtg gactcaggga ggcccagggc tcctctggtc ccaagcgaag gctcctctgc  1020
     237 ttgggattct tcagacagaa gctgggccag cactgtggac tcctcctggg acagggctgg  1080
     238 gtcctctggc tatttggctg agaaggggcc aggccaaggg ccgggtgggg atgggcacca 1140
     239 agaatctctc ccaccacctg aattctccaa ggactcgggt ttcctggaag agctcccaga 1200
     240 agataacctc tcctcctggg ccacctgggg caccttacca ccggagccga atctggtccc 1260
     241 tgggggaccc ccagtttctc ttcagacact gaccttctgc tgggaaagca gccctgagga 1320
E--> 242 ggaagaggag gcgagggaat cagaaattga ggacagcgat gcgggcagct gggggggctga
     243 1380
E--> 244 gagcacccag aggaccgagg acaggggccg gacattgggg cattacatgg ccaggtgagc
     245 1440
     246 tgtcccccga catcccaccg aatctgatg 1469
     250 <210> SEQ ID NO: 10
     251 <211> LENGTH: 244
```

same

move totals up

RAW SEQUENCE LISTING DATE: 08/29/2002
PATENT APPLICATION: US/10/026,106B TIME: 13:29:11

Input Set : A:\EP.txt
Output Set: N:\CRF3\08292002\J026106B.raw

```
     252 <212> TYPE: PRT
     253 <213> ORGANISM: Homo sapiens
W--> 254 <220> FEATURE:
W--> 255 <400> SEQUENCE: 10
     257 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
E--> 258 1                               5                              10
E--> 259 15
     260 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
E--> 261                         20                              25
E--> 262 30
     263 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
E--> 264               35                              40
E--> 265 45
     266 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
E--> 267         50                              55                          60
     268 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
E--> 269 65                              70                                  75
E--> 270 80
     271 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 272                             85                                  90
E--> 273 95
     274 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 275                       100                             105
E--> 276 110
     277 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 278              115                             120                         125
     279 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 282        130                             135                         140
     283 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 284 145                             150                             155
E--> 285 160
     286 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 287                             165                             170
E--> 288 175
     289 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
E--> 290                       180                             185
E--> 291 190
     292 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
E--> 293              195                             200                         205
     294 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Gly
E--> 295        210                             215                         220
     296 Leu Phe Trp Thr His Thr Pro Cys Gly Asn Leu Ser Ala Gln Gln Thr
E--> 297 225                             230                             235
E--> 298 240
     299 Arg Val Arg Glu
```

misaligned amino acid numbering

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/29/2002
PATENT APPLICATION: **US/10/026,106B** TIME: 13:29:12

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\08292002\J026106B.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:7; Line(s) 90
Seq#:8; Line(s) 116,119,127,132,135,146,149,156,159,162,169,172,175,182,187
Seq#:8; Line(s) 190,198,201,204,206
Seq#:9; Line(s) 229,233
Seq#:10; Line(s) 258,261,269,272,275,278,284,287,290,297

VERIFICATION SUMMARY DATE: 08/29/2002
PATENT APPLICATION: **US/10/026,106B** TIME: 13:29:12

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\08292002\J026106B.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:283 W: Missing Blank Line separator, <400> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:46 M:283 W: Missing Blank Line separator, <220> field identifier
L:47 M:283 W: Missing Blank Line separator, <400> field identifier
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:4
L:48 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:19 SEQ:4
L:54 M:283 W: Missing Blank Line separator, <220> field identifier
L:55 M:283 W: Missing Blank Line separator, <400> field identifier
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:63 M:283 W: Missing Blank Line separator, <400> field identifier
L:70 M:283 W: Missing Blank Line separator, <220> field identifier
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:79 M:254 E: No. of Bases conflict, LENGTH:Input:420 Counted:419 SEQ:7
M:254 Repeated in SeqNo=7
L:113 M:283 W: Missing Blank Line separator, <220> field identifier
L:114 M:283 W: Missing Blank Line separator, <400> field identifier
L:116 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:207 M:252 E: No. of Seq. differs, <211> LENGTH:Input:522 Found:512 SEQ:8
L:213 M:283 W: Missing Blank Line separator, <220> field identifier
L:214 M:283 W: Missing Blank Line separator, <400> field identifier
L:229 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:840 SEQ:9
M:254 Repeated in SeqNo=9
L:254 M:283 W: Missing Blank Line separator, <220> field identifier
L:255 M:283 W: Missing Blank Line separator, <400> field identifier
L:258 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:305 M:283 W: Missing Blank Line separator, <220> field identifier
L:306 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:283 W: Missing Blank Line separator, <220> field identifier
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:321 M:283 W: Missing Blank Line separator, <220> field identifier
L:322 M:283 W: Missing Blank Line separator, <400> field identifier
L:331 M:283 W: Missing Blank Line separator, <220> field identifier
L:332 M:283 W: Missing Blank Line separator, <400> field identifier
L:340 M:283 W: Missing Blank Line separator, <220> field identifier
L:341 M:283 W: Missing Blank Line separator, <400> field identifier
L:348 M:283 W: Missing Blank Line separator, <220> field identifier
L:349 M:283 W: Missing Blank Line separator, <400> field identifier
L:356 M:283 W: Missing Blank Line separator, <220> field identifier
L:357 M:283 W: Missing Blank Line separator, <400> field identifier
L:364 M:283 W: Missing Blank Line separator, <220> field identifier
L:365 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY DATE: 08/29/2002
PATENT APPLICATION: **US/10/026,106B** TIME: 13:29:12

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\08292002\J026106B.raw**

L:374 M:283 W: Missing Blank Line separator, <220> field identifier
L:375 M:283 W: Missing Blank Line separator, <400> field identifier